

RAW SEQUENCE LISTING

DATE: 11/20/2000

PATENT APPLICATION: US/09/698,419

TIME: 14:16:10

Input Set : A:\Pto.amc

Output Set: N:\CRF3\11202000\I698419.raw

p5

4 <110> APPLICANT: Vogeli, Gabriel
5 Wood, Linda S.
6 Merchant, Kalpana
8 <120> TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
10 <130> FILE REFERENCE: 28341/6276NCP
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/698,419
C--> 13 <141> CURRENT FILING DATE: 2000-10-27
15 <150> PRIOR APPLICATION NUMBER: US 09/481,794
16 <151> PRIOR FILING DATE: 2000-01-12
18 <150> PRIOR APPLICATION NUMBER: US 09/454,399
19 <151> PRIOR FILING DATE: 1999-12-03
21 <150> PRIOR APPLICATION NUMBER: US 09/429,517
22 <151> PRIOR FILING DATE: 1999-10-28
24 <150> PRIOR APPLICATION NUMBER: US 09/429,555
25 <151> PRIOR FILING DATE: 1999-10-28
27 <150> PRIOR APPLICATION NUMBER: US 09/429,676
28 <151> PRIOR FILING DATE: 1999-10-28
30 <150> PRIOR APPLICATION NUMBER: US 09/429,695
31 <151> PRIOR FILING DATE: 1999-10-28
33 <150> PRIOR APPLICATION NUMBER: US 09/428,114
34 <151> PRIOR FILING DATE: 1999-10-27
36 <150> PRIOR APPLICATION NUMBER: US 09/428,020
37 <151> PRIOR FILING DATE: 1999-10-27
39 <150> PRIOR APPLICATION NUMBER: US 09/427,859
40 <151> PRIOR FILING DATE: 1999-10-27
42 <150> PRIOR APPLICATION NUMBER: US 09/427,653
43 <151> PRIOR FILING DATE: 1999-10-27
45 <160> NUMBER OF SEQ ID NOS: 75
47 <170> SOFTWARE: PatentIn Ver. 2.0
49 <210> SEQ ID NO: 1
50 <211> LENGTH: 1308
51 <212> TYPE: DNA
52 <213> ORGANISM: Homo sapiens
54 <220> FEATURE:
55 <221> NAME/KEY: CDS
56 <222> LOCATION: (157)..(1122)
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (1)
61 <223> OTHER INFORMATION: N = A or C or G or T
64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <222> LOCATION: (1237)
67 <223> OTHER INFORMATION: N = A or C or G or T
69 <220> FEATURE:
70 <221> NAME/KEY: misc_feature
71 <222> LOCATION: (1274)

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72 <223> OTHER INFORMATION: N = A or C or G or T

74 <400> SEQUENCE: 1

W--> 75 ntggttgttg gaccattaaa atgcattatg gaatttttaa aagttggggg agagggagac 60
 77 agtaaaaaata acctatattt tctcttgttt tttttttttt aactctagga aagcccagac 120
 79 aaattttgag ctatttcata acctaccaga cttatc atg cta aca ctg aat aaa 174
 80 Met Leu Thr Leu Asn Lys
 81 1 5
 83 aca gac cta ata cca gct tca ttt att ctg aat gga gtc cca gga ctg 222
 84 Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu Asn Gly Val Pro-Gly Leu
 85 10 15 20
 87 gaa gac aca caa ctc tgg att tcc ttc cca ttc tgc tct atg tat gtt 270
 88 Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro Phe Cys Ser Met Tyr Val
 89 25 30 35
 91 gtg gct atg gta ggg aat tgt gga ctc ctc tac ctc att cac tat gag 318
 92 Val Ala Met Val Gly Asn Cys Gly Leu Leu Tyr Leu Ile His Tyr Glu
 93 40 45 50
 95 gat gcc ctg cac aaa ccc atg tac tac ttc ttg gcc atg ctt tcc ttt 366
 96 Asp Ala Leu His Lys Pro Met Tyr Tyr Phe Leu Ala Met Leu Ser Phe
 97 55 60 65 70
 99 act gac ctt gtt atg tgc tct agt aca atc cct aaa gcc ctc tgc atc 414
 100 Thr Asp Leu Val Met Cys Ser Ser Thr Ile Pro Lys Ala Leu Cys Ile
 101 75 80 85
 103 ttc tgg ttt cat ctc aag gac att gga ttt gat gaa tgc ctt gtc cag 462
 104 Phe Trp Phe His Leu Lys Asp Ile Gly Phe Asp Glu Cys Leu Val Gln
 105 90 95 100
 107 atg ttc ttc atc cac acc ttc aca ggg atg gag tct ggg gtg ctt atg 510
 108 Met Phe Phe Ile His Thr Phe Thr Gly Met Glu Ser Gly Val Leu Met
 109 105 110 115
 111 ctt atg gcc ctg gat cgc tat gtg gcc atc tgc tac ccc tta cgc tat 558
 112 Leu Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr
 113 120 125 130
 115 tca act atc ctc acc aat cct gta att gca aag gtt ggg act gcc acc 606
 116 Ser Thr Ile Leu Thr Asn Pro Val Ile Ala Lys Val Gly Thr Ala Thr
 117 135 140 145 150
 119 ttc ctg aga ggg gta tta ctc att att ccc ttt act ttc ctc acc aag 654
 120 Phe Leu Arg Gly Val Leu Leu Ile Ile Pro Phe Thr Phe Leu Thr Lys
 121 155 160 165
 123 cgc ctg ccc tcc tgc aga ggc aat ata ctt ccc cat acc tac tgt gac 702
 124 Arg Leu Pro Ser Cys Arg Gly Asn Ile Leu Pro His Thr Tyr Cys Asp
 125 170 175 180
 128 cac atg tct gta gcc aaa ttg tcc tgt ggt aat gtc aag gtc aat gcc 750
 129 His Met Ser Val Ala Lys Leu Ser Cys Gly Asn Val Lys Val Asn Ala
 130 185 190 195
 132 atc tat ggt ctg atg gtt gcc ctc ctg att ggg ggc ttt gac ata ctg 798
 133 Ile Tyr Gly Leu Met Val Ala Leu Leu Ile Gly Gly Phe Asp Ile Leu
 134 200 205 210
 136 tgt atc acc atc tcc tat acc atg att ctc cgg gca gtg gtc agc ctc 846
 137 Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu Arg Ala Val Val Ser Leu
 138 215 220 225 230

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```

140 tcc tca gca gat gct cgg cag aag gcc ttt aat acc tgc act gcc cac      894
141 Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe Asn Thr Cys Thr Ala His
142                235                240                245
144 att tgt gcc att gtt ttc tcc tat act cca gct ttc ttc tcc ttc ttt      942
145 Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro Ala Phe Phe Ser Phe Phe
146                250                255                260
148 tcc cac cgc ttt ggg gaa cac ata atc ccc cct tct tgc cac atc att      990
149 Ser His Arg Phe Gly Glu His Ile Ile Pro Pro Ser Cys His Ile Ile
150                265                270                275
152 gta gcc aat att tat ctg ctc cta cca ccc act atg aac cct att gtc      1038
153 Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro Thr Met Asn Pro Ile Val
154                280                285                290
156 tat ggg gtg aaa acc aaa cag ata cga gac tgt gtc ata agg atc ctt      1086
157 Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp Cys Val Ile Arg Ile Leu
158 295                300                305                310
160 tca ggt tct aag gat acc aaa tcc tac agc atg tga atgaacactt      1132
161 Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser Met
162                315                320
164 gccaggagtg agaagagaag gaaagaatta ctctatttg cctctatgc aggagttcat 1192
W--> 166 aaaatctttc tggagttact gtattgatca caaaatggag tttgtgact ggtgcattct 1252
W--> 168 caataagta cttgggaatc tnacatcact ggaaggccca ccacatttct ataat 1308
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 321
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
177 Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu
178 1 5 10 15
180 Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro
181 20 25 30
183 Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu
184 35 40 45
186 Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe
187 50 55 60
189 Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile
190 65 70 75 80
192 Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe
193 85 90 95
195 Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met
196 100 105 110
198 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
199 115 120 125
201 Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala
202 130 135 140
204 Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro
205 145 150 155 160
207 Phe Thr Phe Leu Thr Lys Arg Leu Pro Ser Cys Arg Gly Asn Ile Leu
208 165 170 175
210 Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly

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```

211          180          185          190
213 Asn Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
214          195          200          205
216 Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
217          210          215          220
219 Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
220 225          230          235          240
222 Asn Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro
223          245          250          255
225 Ala Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro
226          260          265          270
228 Pro Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro
229          275          280          285
231 Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp
232          290          295          300
234 Cys Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser
235 305          310          315          320
237 Met
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 1014
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: CDS
246 <222> LOCATION: (1)..(1014)
248 <400> SEQUENCE: 3
249 atg gat gaa aca gga aat ctg aca gta tct tct gcc aca tgc cat gac 48
250 Met Asp Glu Thr Gly Asn Leu Thr Val Ser Ser Ala Thr Cys His Asp
251 1 5 10 15
255 act att gat gac ttc cgc aat caa gtg tat tcc acc ttg tac tct atg 96
256 Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met
257 20 25 30
259 atc tct gtt gta ggc ttc ttt ggc aat ggc ttt gtg ctc tat gtc ctc 144
260 Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu
261 35 40 45
263 ata aaa acc tat cac aag aag tca gcc ttc caa gta tac atg att aat 192
264 Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn
265 50 55 60
267 tta gca gta gca gat cta ctt tgt gtg tgc aca ctg cct ctc cgt gtg 240
268 Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val
269 65 70 75 80
271 gtc tat tat gtt cac aaa ggc att tgg ctc ttt ggt gac ttc ttg tgc 288
272 Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys
273 85 90 95
275 cgc ctc agc acc tat gct ttg tat gtc aac ctc tat tgt agc atc ttc 336
276 Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe
277 100 105 110
279 ttt atg aca gcc atg agc ttt ttc cgg tgc att gca att gtt ttt cca 384
280 Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro

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```

281      115      120      125
283 gtc cag aac att aat ttg gtt aca cag aaa aaa gcc agg ttt gtg tgt 432
284 Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys
285      130      135      140
287 gta ggt att tgg att ttt gtg att ttg acc agt tct cca ttt cta atg 480
288 Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met
289 145      150      155      160
291 gcc aaa cca caa aaa gat gag aaa aat aat acc aag tgc ttt gag ccc 528
292 Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro
293      165      170      175
295 cca caa gac aat caa act aag aat cat gtt ttg gtc ttg cat tat gtg 576
296 Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val
297      180      185      190
299 tca ttg ttt gtt ggc ttt atc atc cct ttt gtt att ata att gtc tgt 624
300 Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Val Cys
301      195      200      205
303 tac aca atg atc att ttg acc tta cta aaa aaa tca atg aaa aaa aat 672
304 Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn
305      210      215      220
307 ctg tca agt cat aaa aag gct ata gga atg atc atg gtc gtg acc gct 720
308 Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala
309 225      230      235      240
311 gcc ttt tta gtc agt ttc atg cca tat cat att caa cgt acc att cac 768
312 Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His
313      245      250      255
315 ctt cat ttt tta cac aat gaa act aaa ccc tgt gat tct gtc ctt aga 816
316 Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg
317      260      265      270
319 atg cag aag tcc gtg gtc ata acc ttg tct ctg gct gca tcc aat tgt 864
320 Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys
321      275      280      285
323 tgc ttt gac cct ctc cta tat ttc tct ggg ggt aac ttt agg aaa 912
324 Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys
325      290      295      300
327 agg ctg tct aca ttt aga aag cat tct ttg tcc agc gtg act tat gta 960
328 Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val
329 305      310      315      320
331 ccc aga aag aag gcc tct ttg cca gaa aaa gga gaa gaa ata tgt aaa 1008
332 Pro Arg Lys Lys Ala Ser Leu Pro Glu Lys Gly Glu Glu Ile Cys Lys
333      325      330      335
335 gta tag 1014
336 Val
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 337
341 <212> TYPE: PRT
342 <213> ORGANISM: Homo sapiens
344 <400> SEQUENCE: 4
345 Met Asp Glu Thr Gly Asn Leu Thr Val Ser Ser Ala Thr Cys His Asp
346 1 5 10 15

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 11/20/2000

PATENT APPLICATION: US/09/698,419

TIME: 14:16:11

Input Set : A:\Pto.amc

Output Set: N:\CRF3\11202000\I698419.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:2044 M:283 W: Missing Blank Line separator, <220> field identifier

Does Not Comply
Corrected Diskette Needed

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339 <210> SEQ ID NO: 4
340 <211> LENGTH: 337
341 <212> TYPE: PRT
342 <213> ORGANISM: Homo sapiens
E--> 344 <400> SEQUENCE: 204
345 Met Asp Glu Thr Gly Asn Leu Thr Val Ser Ser Ala Thr Cys His Asp
346 1 5 10 15
348 Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met
349 20 25 30
351 Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu
352 35 40 45
354 Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn
355 50 55 60
357 Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/698,419

DATE: 11/13/2000

TIME: 15:48:16

Input Set : A:\6276NCPseq.txt

Output Set: N:\CRF3\11132000\I698419.raw

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358 65          70          75          80
360 Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys
361          85          90          95
363 Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe
364          100          105          110
366 Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro
367          115          120          125
369 Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys
370          130          135          140
372 Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met
373 145          150          155          160
375 Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro
376          165          170          175
378 Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val
379          180          185          190
382 Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Val Cys
383          195          200          205
385 Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn
386          210          215          220
388 Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala
389 225          230          235          240
391 Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His
392          245          250          255
394 Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg
395          260          265          270
397 Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys
398          275          280          285
400 Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys
401          290          295          300
403 Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val
404 305          310          315          320
406 Pro Arg Lys Lys Ala Ser Leu Pro Glu Lys Gly Glu Glu Ile Cys Lys
407          325          330          335
409 Val

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2439 <210> SEQ ID NO: 60

2440 <211> LENGTH: 24

2441 <212> TYPE: DNA

2442 <213> ORGANISM: Artificial Sequence

2444 <220> FEATURE:

2445 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer LW1440

2447 <400> SEQUENCE: 60

E--> 2448 aagcggatgt ttagacctct tgtg

2449 24

24

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/698,419

DATE: 11/13/2000

TIME: 15:48:18

Input Set : A:\6276NCPseq.txt

Output Set: N:\CRF3\11132000\I698419.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:344 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:2
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:1176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:2044 M:283 W: Missing Blank Line separator, <220> field identifier
L:2448 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:60